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# Discretizing the $SI$ Epidemic Model

Kacie M. Sutton

**Abstract.** Epidemic models are used as a tool to analyze the behaviors of biological diseases and how they spread. In the $SI$ epidemic model, where $S$ represents the group of susceptibles and $I$ represents the group of infectives, the numerical outputs can be nonintegers, which creates obstacles in applying these results to our biological reality. Here, we discretize the model output values by applying various combinations of integerizing (Round, Ceiling, Floor). These discretized values allow the results of the $SI$ model to be applied to reality in terms of whole person outputs. Nine potential discretized $SI$ models are formed with the combinations of integerizing. We eliminate several of these potential models because they do not meet the fundamental property of the $SI$ model – fixed population size. We compare the properties of the three models that meet the fundamental property with the properties of the original (nondiscretized) $SI$ model. Several unexpected results appear, such as a basic reproduction number, $R_0$, for two of the three discretized models; the original $SI$ model has no such $R_0$ value.

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# 1 Introduction

Mathematical epidemiology has been used in order to understand how epidemics spread and to predict important disease properties, such as the total number who become infected. There are different classic disease models that have been studied, such as the $SI$ (susceptible-infected), the $SIS$ (susceptible-infected-susceptible), and the $SIR$ (susceptible-infected-recovered) models, which help us understand epidemics in a population. In each such model the population is partitioned into the $S$ class of individuals who are not yet infected, the $I$ class of individuals who are infected, and possibly the $R$ class of individuals who are recovered from the disease. Then a system of difference equations is given that describes how individuals move between classes. For example, when an individual becomes infected, the model equations would force the number in the $S$ class to decrease and the number in the $I$ class to increase.

In this paper, we will be working with the $SI$ epidemic model. The $SI$ model splits the population into two groups, the susceptible individuals who may contract the disease and the infected individuals who may spread the disease to the susceptibles. Once a susceptible becomes infected, he or she moves into the infected group, increasing the size of the infected class and decreasing the size of the susceptible class.

In the $SI$ model, we assume that each person in the susceptible population is equally likely to be transmitted the disease through contact with an infected individual. Once a person is infected, they cannot recover; they remain in the $I$ class forever ([1]). Also, we assume that the length of the disease outbreak is short compared with the average person's lifespan, so death is not a factor ([3]). Therefore, this model can be applied to diseases for which individuals never recover and for which disease spread is relatively quick, such as herpes (HSV-1 or HSV-2) caused by the virus *Herpesviridae*.

In the $SI$ epidemic model with discrete time, the number of individuals in the susceptible and infective populations at time $(n+1)\Delta t$, can be represented with the following two difference equations.

$$S_{n+1} = S_n \left(1 - \frac{\alpha \Delta t}{N} I_n\right) \tag{1}$$

$$I_{n+1} = I_n \left(1 + \frac{\alpha \Delta t}{N} S_n\right), \tag{2}$$

where the rate of contact between the susceptible and infective populations that allows the susceptibles to become infected per unit time is $\alpha$, the fixed time step is $\Delta t$, and $N$ is the total population size. All three parameters $\alpha$, $\Delta t$, and $N$ must be positive. The time step $\Delta t$ has to be less than the average time required for transmission. The initial conditions for the disease spread are given by $S_0$ and $I_0$, the number of susceptible and infected individuals at time $n = 0$. We assume that $S_0 + I_0 = N$ with $0 \leq S_0 \leq N$ and $0 \leq I_0 \leq N$.

Even given integer initial conditions, the $SI$ model outputs will be nonintegers. The goal of this paper is to discretize the $SI$ model outputs to ensure whole person output values. Throughout the paper we will be working with the discrete time $SI$ model with time denoted

by subscript $n$. We use the phrase discretized model to mean the discrete time $SI$ model with discrete whole person outputs. The phrase nondiscretized model is used to indicate the original discrete time $SI$ model with noninteger outputs.

The idea to study a population model with discretized model outputs came from Henson, et al. ([2]). In their work, the authors note that animals and plants are counted in discrete units, but many population models that show interesting (chaotic) behavior have noninteger outputs. They compare the model outputs of a nondiscretized and a discretized Ricker population model with data from a population experiment of the flour beetle *Tribolium* in order to determine which model best matches the experimental data. Their conclusion is that neither the nondiscretized nor the discretized model can completely account for the data. The authors believe that the population data is best modeled by a stochastic (random) blending of the two models.

We begin in Section 2 with a description of the properties of the discrete time (nondiscretized) $SI$ model. In Section 3 we present the three possible integerizations of the model outputs and discuss the nine resulting discretized $SI$ models. We present the properties of the nondiscretized $SI$ models in Section 3.1. We show numerical trials performed for the nondiscretized and the discretized $SI$ model(s) in Section 4. Finally, in Section 5 we discuss our conclusions and future work.

# 2 Preliminaries

We start with a catalogue of the properties of the (nondiscretized) $SI$ model. Some properties we want to change, most importantly the noninteger outputs. Those we consider fundamental (fixed population size and monotonicity) will be required when we discretize the model outputs. The others (positivity, an $R_0$ value, and equilibrium points) will be examined in detail for the discretized models that meet the fundamental properties.

### Noninteger outputs

The first property is the one that does not match our biological reality of whole persons. In the $SI$ model, the values of $S_n$ and $I_n$ are not necessarily integers. For example, with $\alpha = 0.67$ and all other model parameters as in Table 5, the numerical $SI$ model outputs include

$$S = \{99,\ 98.3367,\ 97.2408,\ 95.4432,\ \dots\} \text{ and}$$
$$I = \{1,\ 1.6633,\ 2.75918,\ 4.55681,\ \dots\}.$$

We will discretize the $SI$ model in order to change this property.

### Fixed population size

The total population size of the $SI$ model is constant. We know this because $S_{n+1} + I_{n+1} = S_n + I_n$, for every $n$. Therefore, the population size $N$ is constant. This property is funda-

mental and will be required for the discretized models.

### Monotonicity

In the $SI$ model, the number of susceptible individuals decreases monotonically, that is $S_{n+1} \leq S_n$, for all $n$. We also have that the number of infected individuals increases monotonically, that is $I_{n+1} \geq I_n$, for all $n$. Monotonicity can be seen from the model equations. The equation for $S_{n+1}$ is $S_n$ less a non-negative value, so $S_{n+1}$ is less than or equal to $S_n$ for every $n$. Note that the monotonicity of $S_n$ and $I_n$ is strict when $S_0 < N$. We will require the discretized models to be monotonic.

### Positivity

Positivity means that under certain conditions on the model parameters the number of susceptible individuals stays between 0 and $N$, as does the number of infected individuals, for every $n$. The positivity property for the nondiscretized $SI$ model can be stated as follows.

**Theorem 1.** *The number of susceptible individuals is never negative, $S_n \geq 0$, and the number of infected individuals is never more than the total population size, $I_n \leq N$, for every $n$, if and only if $\alpha\Delta t \leq 1$ ([1]).*

In all of our models we will require the positivity condition to hold. As we show below, each of the discretized models has a different condition that guarantees positivity of the model outputs.

### An $R_0$ value

**Definition 1.** In a disease model, the basic reproduction number, $R_0$, is a certain combination of the model parameters such that if $R_0 > 1$, then the disease will spread ($I_n$ increases), and if $R_0 < 1$, then the disease will not spread ([4]).

The traditional definition states that the $R_0$ value is a combination of model parameters such that if $R_0 > 1$, then $I_n$ will increase, while if $R_0 < 1$, then $I_n$ will decrease. For the discretized models, we find that either the disease will spread, $I_n$ increases, or $I_n = I_{n+1}$, for all $n$. In particular, the number of infected individuals does not decrease with $R_0 < 1$. Thus we have modified the traditional definition.

There is no basic reproduction number, $R_0$, for the nondiscretized $SI$ model; once the disease has entered the population, everyone will become infected.

### Equilibrium Points

The points of equilibrium represent when both populations, $S_n$ and $I_n$, attain balance and cease to decrease or increase.

**Definition 2.** An equilibrium point for the $SI$ model is a point $(S^*, I^*)$ such that plugging these points into the $SI$ model equations outputs the same point $(S^*, I^*)$.

There are two equilibrium points for the nondiscretized $SI$ model. First, $(N, 0)$, meaning there never were any infected individuals, and second $(0, N)$, meaning the entire population becomes infected ([1]).

For the $SI$ model, if there is at least one infected individual, then the equilibrium point $(0, N)$ means that the "entire" population will become infected. This is not quite true, because the number of susceptible individuals will approach 0 asymptotically but never reach 0.

**Summary**

In summary, we want to change the noninteger outputs property of the original $SI$ model to produce discretized $SI$ models. We require two fundamental properties to be met for the discretized $SI$ models – fixed population size and monotonicity. The three properties of positivity, an $R_0$ value, and equilibrium points are shown to depend on the form of the discretized model.

# 3 Theoretical Results

It is clear that in the case of the $SI$ epidemic model, the numerical outputs for the susceptible population and the infective population can be nonintegers. This is problematic because we need whole number outputs to be compatible with the biological reality of whole persons. In order to do this, we need to apply some form of integerizing to the outputs to make it applicable to reality.

Inspired by the work of Henson, et al. ([2]), who examined the integerization of a population (logistic) model, we alter the original $SI$ model by discretizing the outputs of the model at each time step and use the resulting integers as initial conditions for the next time step. This models the situation where there are contacts during the day, then individuals return home, and the next day there are an integer number of susceptible and infected individuals who are in contact. The discretizing forces the outputs to be whole numbers so that we can apply the model to real life situations. We consider nine different potential discretized models, formed by the three types of integerizing applied to the susceptible and infective populations separately:

- Round: all numbers in the interval $[n-0.5, n+0.5)$ are discretized to $n$. When Round is applied, the number discretizes to the closest integer.

- Floor: all numbers in the interval $[n, n+1)$ are discretized to $n$. Floor forces the number to discretize to the greatest integer less than the number.

- Ceiling: all numbers in the interval $(n-1, n]$ are discretized to $n$. When a number is forced to discretize to the next highest integer, that is considered Ceiling the number.

For example, to floor the susceptible population and ceiling the infected population, we mean the new $SI$ model

$$S_{n+1} = \text{Floor}\left[S_n\left(1 - \frac{\alpha\Delta t}{N} I_n\right)\right] \tag{3}$$

$$I_{n+1} = \text{Ceiling}\left[I_n\left(1 + \frac{\alpha\Delta t}{N} S_n\right)\right]. \tag{4}$$

There are nine discretized $SI$ models, each of which produce integer outputs for every $n$. However, not every combination of discretizing satisfies the property of fixed population size. The nine possible combinations of discretizing are portrayed in Table 1 along with the value of $S + I$ compared to $N$.

| Type of Discretizing for $S$ | Type of Discretizing for $I$ | $S + I$ |
|---|---|---|
| Round | Round | Equals N (*) |
| Round | Ceiling | Greater than N |
| Round | Floor | Less than N |
| Ceiling | Round | Greater than N |
| Ceiling | Ceiling | Greater than N |
| Ceiling | Floor | Equals N |
| Floor | Round | Less than N |
| Floor | Ceiling | Equals N |
| Floor | Floor | Less than N |

Table 1: The different types of discretizing, each guarantees the model outputs are whole persons. The value of $S + I$ compared to $N$. We are checking to ensure the population adds up the the total population, $N$. (*) See the last paragraph before Section 3.1.

There are only three combinations of discretizing that satisfy the fixed population size property - Round both populations, Ceiling the susceptibles combined with Floor the infectives, and Floor the susceptibles combined with Ceiling the infectives. The rest of the models with different arrangements of discretizing do not keep a constant total population. We will be focusing on the three successful combinations, so we will call them Model I, Model II, and Model III; Model I representing the Round model, Model II representing the model of Ceiling the susceptibles and Floor the infectives, and Model III representing the model including both Floor the susceptibles and Ceiling the infectives.

Some care must be taken with Model I, the rounding model. For example, if the pre-rounded number of susceptible individuals is 32.5 and the pre-rounded number of infected

individuals is 67.5 (meaning $N = 100$), then both populations will round up to 33 and 68, respectively. Adding these discretized values gives $101 \neq N$. This is a common problem when numerically working with rounding. In this case, we round up the value that is over $N/2$ and round down the value that is below $N/2$. So we would have 32 susceptibles and 68 infecteds.

## 3.1 Properties of the Discretized SI Models

By construction, Model I, Model II, and Model III have integer outputs taking care of the noninteger outputs property of the original $SI$ model. Also, these three models were chosen because they satisfy the fixed population size property.

The other fundamental property that we require for the discretized $SI$ models is the monotonicity property. This property holds for the discretized $SI$ models using an argument similar to that for the original $SI$ model.

**Theorem 2.** *All three of the discretized $SI$ models have the monotonicity property, that is $S_{n+1} \leq S_n$ and $I_{n+1} \geq I_n$, for all $n$.*

*Proof.* Set $S_m$ to be the discretized model output using any of the three models, and set $S^*_{m+1}$ to be the non-discretized value $S_m\left(1 - \dfrac{\alpha \Delta t I_m}{N}\right)$. Because $I_m \geq 0$, we know that $S^*_{m+1}$ is less than or equal to $S_m$, that is $S^*_{m+1} \leq S_m$. Applying Round, Ceiling, or Floor preserves the inequality "less than or equal to", so we have that the model output using any of the three models (Model I, Model II, Model III) satisfies $S_{m+1} \leq S_m$. Thus the discretized models are monotonic. □

For the original $SI$ model with $S_0 < N$ the monotonicity is strict, meaning $S_{n+1} < S_n$. Whether or not the discretized $SI$ models are strictly monotone depends on the $R_0$ value. See Sections 3.1.1 and 3.1.2 for more details.

We examine the other three properties of the original $SI$ model – positivity, an $R_0$ value, and equilibrium points – for each of the three discretized $SI$ models.

### 3.1.1 Model I: Round $S$, Round $I$

The properties of Model I are similar to those of Model II, and quite different than those of the original $SI$ model and of Model III. We begin by giving the positivity property.

**Theorem 3.** *The number of susceptible individuals is never negative, $S_n \geq 0$, and the number of infected individuals is never more than the total population size, $I_n \leq N$, for every $n$, if and only if $\alpha \Delta t \leq \min\limits_n \left[\left(1 + \dfrac{1}{2S_n}\right)\dfrac{N}{I_n}\right]$.*

*Proof.* First, assume that $S_n \geq 0$ and $I_n \leq N$ for every $n$. Thus for $m \in \mathbb{N}$, we know that

$$0 \leq S_m = \text{Round}\left[S_{m-1}\left(1 - \frac{\alpha \Delta t I_{m-1}}{N}\right)\right].$$

In order for a number to Round to an integer of 0 or higher, the number must be greater than or equal to $-1/2$. Thus

$$\frac{-1}{2} \leq S_{m-1}\left(1 - \frac{\alpha \Delta t I_{m-1}}{N}\right).$$

Solving for $\alpha\Delta t$ gives

$$\alpha\Delta t \leq \left(1 + \frac{1}{2S_{m-1}}\right)\frac{N}{I_{m-1}}.$$

This must be true for every $m \in \mathbb{N}$. Thus we must have that

$$\alpha\Delta t \leq \min_n \left[\left(1 + \frac{1}{2S_n}\right)\frac{N}{I_n}\right].$$

Now, assume that $\alpha\Delta t \leq \min_n \left[\left(1 + \frac{1}{2S_n}\right)\frac{N}{I_n}\right]$. We proceed with induction. For the initial conditions $S_0$ and $I_0$, we know that $S_0 \geq 0$ and $I_0 \leq N$. Assume that $S_j \geq 0$ and $I_j \leq 0$ for $j = 0, 1, \ldots, m$. We want to show that $S_{m+1} \geq 0$ and $I_{m+1} \leq N$.

Because $\alpha\Delta t \leq \min_n \left[\left(1 + \frac{1}{2S_n}\right)\frac{N}{I_n}\right]$, we know that

$$\alpha\Delta t \leq \left(1 + \frac{1}{2S_m}\right)\frac{N}{I_m}.$$

Rearranging gives that

$$\frac{-1}{2} \leq S_m\left(1 - \frac{\alpha \Delta t I_m}{N}\right).$$

Rounding both sides of the inequality preserves the inequality, so we have

$$\text{Round}\left[\frac{-1}{2}\right] \leq \text{Round}\left[S_m\left(1 - \frac{\alpha \Delta t I_m}{N}\right)\right].$$

This implies that $0 \leq S_{m+1}$ and, because of the fixed population size property, this also implies that $N \geq I_{m+1}$. □

Model I does have a basic reproduction number. This is different than the original $SI$ model because the original $SI$ model has no $R_0$ value. We state the case of disease spread as $S_1 < S_0$. We cannot say that $S_{n+1} < S_n$ for every $n$ because when the susceptible population reaches 0 the number of susceptibles will stay at 0.

**Theorem 4.** *Let* $R_0 = \dfrac{2\alpha\Delta t I_0 S_0}{N}$. *If* $R_0 \leq 1$, *then the disease does not spread, that is* $S_{n+1} = S_n$ *for every* $n$. *If* $R_0 > 1$, *then the disease does spread, that is* $S_1 < S_0$.

*Proof.* For the disease to not spread we require that $S_1 = S_0$. In particular, we must have

$$S_1 = \text{Round}\left[S_0\left(1 - \frac{\alpha \Delta t I_0}{N}\right)\right] = S_0.$$

Thus to not have disease spread with Round we must have

$$S_0 - \frac{1}{2} \leq S_0\left(1 - \frac{\alpha \Delta t I_0}{N}\right).$$

Simplifying gives

$$\frac{2\alpha \Delta t I_0 S_0}{N} \leq 1.$$

Similarly, for the disease to spread with rounding we must have

$$S_0\left(1 - \frac{\alpha \Delta t I_0}{N}\right) < S_0 - \frac{1}{2},$$

which gives

$$\frac{2\alpha \Delta t I_0 S_0}{N} > 1.$$

□

Finally, we give the equilibrium points for Model I. The equilibrium points depend on the $R_0$ value.

**Theorem 5.** *If $R_0 \leq 1$, then the equilibrium points are $(S_0, I_0)$ for any initial conditions $0 \leq S_0 \leq N$ and $0 \leq I_0 \leq N$.*

*If $R_0 > 1$, then for initial conditions $S_0 = N$ and $I_0 = 0$ the equilibrium point is $(N, 0)$, and for any initial conditions $0 \leq S_0 < N$ and $0 < I_0 \leq N$ the equilibrium point is $(0, N)$.*

*Proof.* Assume that $R_0 \leq 1$, then the disease does not spread meaning $S_1 = S_0$. This implies that $S_n = S_0$, for all $n$. By the fixed population size property, we also have that $I_n = I_0$, for all $n$. Thus the equilibrium point is $(S_0, I_0)$.

Now assume that $R_0 \geq 1$. To verify that $(N, 0)$ is an equilibrium point we simply plug these values into the model equations as the initial conditions. We find that $S_n = N$ and $I_n = 0$, for all $n$. Similarly, it is possible to show that $(0, N)$ is also an equilibrium point.

In order to verify that there are no other equilibrium points when $R_0 \geq 1$, we verify that if $S_0 \neq N$, then $S_{m+1} < S_m$ until the time when $S_n = 0$. Let $n$ be the least integer with $S_n = 0$, and choose any $m < n$. Consider

$$S_{m+1} = \text{Round}\left[S_m\left(1 - \frac{\alpha \Delta t I_m}{N}\right)\right].$$

In order for $S_{m+1}$ to be strictly less than $S_m$ using Round, we must have that

$$S_m\left(1 - \frac{\alpha \Delta t I_m}{N}\right) < S_m - \frac{1}{2}.$$

Simplifying gives that we must have

$$1 < \frac{2\alpha\Delta t I_m S_m}{N} = \frac{2\alpha\Delta t (N - S_m) S_m}{N} = f(S_m),$$

for $S_m \in [N - S_0, S_0]$. The function $f$ has one critical point at $S_m = N/2$. The second derivative test verifies that this critical point is at a maximum of $f$. Thus the minimum value of $f$ must be attained at the end points. Both end points give the same minimum value of $f(S_0) = f(N - S_0) = R_0$. We assumed that $R_0 > 1$, and this implies that we do indeed have

$$1 < \frac{2\alpha\Delta t I_m S_m}{N}.$$

Thus $S_{m+1} < S_m$, and using that the integers are discrete, we conclude that there are no other possible equilibrium points when $R_0 > 1$. □

Note that the above proof gives that with $R_0 > 1$ and $S_0 \neq N$, then the discretized $SI$ model is strictly monotone decreasing until the time when $S_n = 0$.

### 3.1.2 Model II: Ceiling $S$, Floor $I$

The properties of Model II are similar to those of Model I. We begin by giving the positivity property.

**Theorem 6.** *The number of susceptible individuals is never negative, $S_n \geq 0$, and the number of infected individuals is never more than the total population size, $I_n \leq N$, for every $n$, if and only if $\alpha\Delta t < \min_n \left[ \left( 1 + \frac{1}{S_n} \right) \frac{N}{I_n} \right]$*

*Proof.* First, assume that $S_n \geq 0$ and $I_n \leq N$ for every $n$. Thus for $m \in \mathbb{N}$, we know that

$$0 \leq S_m = \text{Ceiling} \left[ S_{m-1} \left( 1 - \frac{\alpha\Delta t I_{m-1}}{N} \right) \right].$$

In order for a number to Ceiling to an integer of 0 or higher, the number must be strictly greater than $-1$. Thus

$$-1 < S_{m-1} \left( 1 - \frac{\alpha\Delta t I_{m-1}}{N} \right).$$

Solving for $\alpha\Delta t$ gives

$$\alpha\Delta t < \left( 1 + \frac{1}{S_{m-1}} \right) \frac{N}{I_{m-1}}.$$

This must be true for every $m \in \mathbb{N}$. Thus we must have

$$\alpha\Delta t < \min_n \left[ \left( 1 + \frac{1}{S_n} \right) \frac{N}{I_n} \right]$$

Now, assume that $\alpha\Delta t < \min_n \left[\left(1+\frac{1}{S_n}\right)\frac{N}{I_n}\right]$. We proceed with induction. For the initial conditions $S_0$ and $I_0$, we know that $S_0 \geq 0$ and $I_0 \leq N$. Assume that $S_j \geq 0$ and $I_j \leq 0$ for $j = 0, 1, \ldots, m$. We want to show that $S_{m+1} \geq 0$ and $I_{m+1} \leq N$.

Because $\alpha\Delta t < \min_n \left[\left(1+\frac{1}{S_n}\right)\frac{N}{I_n}\right]$, we know that

$$\alpha\Delta t < \left(1+\frac{1}{S_m}\right)\frac{N}{I_m}.$$

Rearranging gives that

$$-1 < S_m\left(1-\frac{\alpha\Delta t I_m}{N}\right).$$

Because the right-hand side of the inequality is strictly larger than -1, when you Ceiling the right-hand side the result will be a number greater than or equal to 0. So we have

$$0 \leq \text{Ceiling}\left[S_m\left(1-\frac{\alpha\Delta t I_m}{N}\right)\right] = S_{m+1}.$$

Because of the fixed population size property, this also implies that $N \geq I_{m+1}$.

□

Model II does have a basic reproduction number, as with Model I. This is different than the original $SI$ model because the original $SI$ models has no $R_0$ value. Again, we state the case of disease spread as $S_1 < S_0$.

**Theorem 7.** *Let $R_0 = \frac{\alpha\Delta t I_0 S_0}{N}$. If $R_0 < 1$, then the disease does not spread, that is $S_{n+1} = S_n$ for every $n$. If $R_0 \geq 1$, then the disease does spread, that is $S_1 < S_0$.*

*Proof.* For the disease to not spread we must have $S_1 = S_0$. In particular, we must have

$$S_1 = \text{Ceiling}\left[S_0\left(1-\frac{\alpha\Delta t I_0}{N}\right)\right] = S_0.$$

Thus to not have disease spread with Ceiling we must have

$$S_0 - 1 < S_0\left(1-\frac{\alpha\Delta t I_0}{N}\right).$$

Simplifying gives

$$\frac{\alpha\Delta t I_0 S_0}{N} < 1.$$

Similarly, for the disease to spread with Ceiling we must have

$$S_0\left(1-\frac{\alpha\Delta t I_0}{N}\right) \leq S_0 - 1,$$

which gives

$$\frac{\alpha \Delta t I_0 S_0}{N} \geq 1.$$

□

Finally, we give the equilibrium points for Model II. The equilibrium points depend on the $R_0$ value.

**Theorem 8.** *If $R_0 < 1$, then the equilibrium points are $(S_0, I_0)$ for any initial conditions $0 \leq S_0 \leq N$ and $0 \leq I_0 \leq N$.*

*If $R_0 \geq 1$, then for initial conditions $S_0 = N$ and $I_0 = 0$ the equilibrium point is $(N, 0)$, and for any initial conditions $0 \leq S_0 < N$ and $0 < I_0 \leq N$ the equilibrium point is $(0, N)$.*

*Proof.* Assume that $R_0 < 1$, then the disease does not spread, meaning $S_1 = S_0$. This implies that $S_n = S_0$, for all $n$. By the fixed population size property, we also have that $I_n = I_0$, for all $n$. Thus the equilibrium point is $(S_0, I_0)$.

Now assume that $R_0 > 1$. To verify that $(N, 0)$ is an equilibrium point we simply plug these values into the model equations as the initial conditions. We find that $S_n = N$ and $I_n = 0$, for all $n$. Similarly, it is possible to show that $(0, N)$ is also an equilibrium point.

In order to verify that there are no other equilibrium points when $R_0 > 1$, we verify that if $S_0 \neq N$, then $S_{m+1} < S_m$ until the time when $S_n = 0$. Let $n$ be the least integer with $S_n = 0$, and choose any $m < n$. Consider

$$S_{m+1} = \text{Ceiling}\left[S_m\left(1 - \frac{\alpha \Delta t I_m}{N}\right)\right].$$

In order for $S_{m+1}$ to be strictly less than $S_m$ using Ceiling, we must have that

$$S_m\left(1 - \frac{\alpha \Delta t I_m}{N}\right) \leq S_m - 1.$$

Simplifying gives that we must have

$$1 \leq \frac{\alpha \Delta t I_m S_m}{N} = \frac{2\alpha \Delta t (N - S_m) S_m}{N} = f(S_m),$$

for $S_m \in [N - S_0, S_0]$. Arguing as in the case of Round, the function $f$ has one critical point at $S_m = N/2$, which is a maximum. Thus the minimum value of $f$ must be attained at the end points. Both end points give the same minimum value of $f(S_0) = f(N - S_0) = R_0$. We assumed that $R_0 \geq 1$, and this implies that we do indeed have

$$1 \leq \frac{\alpha \Delta t I_m S_m}{N}.$$

Thus $S_{m+1} < S_m$, and using that the integers are discrete, we conclude that there are no other possible equilibrium points when $R_0 \geq 1$. □

### 3.1.3 Model III: Floor $S$, Ceiling $I$

Model III is the discritized $SI$ model whose properteis are most similar to the original $SI$ model. We begin by giving the positivity property.

**Theorem 9.** *The number of susceptible individuals is never negative, $S_n \geq 0$, and the number of infected individuals is never more than the total population size, $I_n \leq N$, for every $n$, if and only if $\alpha\Delta t \leq 1$*

*Proof.* First, assume that $S_n \geq 0$ and $I_n \leq N$ for every $n$. Thus for $m \in \mathbb{N}$, we know that

$$0 \leq S_m = \text{Floor}\left[S_{m-1}\left(1 - \frac{\alpha\Delta t I_{m-1}}{N}\right)\right].$$

In order for a number to floor to an integer of 0 or higher, the number must be greater than or equal to 0. Thus

$$0 \leq S_{m-1}\left(1 - \frac{\alpha\Delta t I_{m-1}}{N}\right).$$

Solving for $\alpha\Delta t$ gives

$$\alpha\Delta t \leq \frac{N}{I_{m-1}}.$$

This must be true for every $m \in \mathbb{N}$. Thus we must have

$$\alpha\Delta t \leq \min_n \left[\frac{N}{I_n}\right].$$

Using that $0 \leq I_n \leq N$, we know that the minimum value of $\dfrac{N}{I_n}$ occurs when $I_n = N$. Thus we must have

$$\alpha\Delta t \leq 1.$$

Now, assume that $\alpha\Delta t \leq 1$. We proceed with induction. For the initial conditions $S_0$ and $I_0$, we know that $S_0 \geq 0$ and $I_0 \leq N$. Assume that $S_j \geq 0$ and $I_j \leq 0$ for $j = 0, 1, \ldots, m$. We want to show that $S_{m+1} \geq 0$ and $I_{m+1} \leq N$.

Because $\alpha\Delta t \leq 1$ and $0 \leq I_n \leq N$, we know that

$$\alpha\Delta t \leq 1 \leq \min_n \left[\frac{N}{I_n}\right].$$

In particular we know that

$$\alpha\Delta t \leq \frac{N}{I_m}.$$

Rearranging gives that

$$0 \leq 1 - \frac{\alpha\Delta t I_m}{N}.$$

Multiplying both sides by the positive value $S_m$ gives

$$0 \leq S_m \left(1 - \frac{\alpha \Delta t I_m}{N}\right).$$

Floor both sides of the inequality preserves the inequality, so we have

$$\text{Floor}\,[0] \leq \text{Floor}\left[S_m \left(1 - \frac{\alpha \Delta t I_m}{N}\right)\right].$$

This implies that $0 \leq S_{m+1}$ and, because of the fixed population size property, this also implies that $N \geq I_{m+1}$. □

Model III does not have a basic reproduction number. This matches the original $SI$ model, which has no $R_0$ value. As soon as there is one infected individual in the population, the disease will spread. This immediately gives us the equilibrium points for Model III, which also matches the equilibrium point property of the original $SI$ model.

**Theorem 10.** *For initial conditions $S_0 = N$ and $I_0 = 0$ the equilibrium point is $(N, 0)$, and for any initial conditions $0 \leq S_0 < N$ and $0 < I_0 \leq N$ the equilibrium point is $(0, N)$.*

*Proof.* To verify that $(N, 0)$ is an equilibrium point we simply plug these values into the model equations as the initial conditions. We find that $S_n = N$ and $I_n = 0$, for all $n$. Similarly, it is possible to show that $(0, N)$ is also an equilibrium point.

In the case of $S_0 < N$, we verify that Model III has strict monotonicity until the time when $S_n = 0$. Let $n$ be the least integer with $S_n = 0$. Consider

$$S_{m+1} = \text{Floor}\left[S_m \left(1 - \frac{\alpha \Delta t I_m}{N}\right)\right].$$

In order for $S_{m+1}$ to be strictly less than $S_m$ using Floor, we must have that

$$S_m \left(1 - \frac{\alpha \Delta t I_m}{N}\right) < S_m.$$

Simplifying gives that we must have

$$0 < \frac{\alpha \Delta t I_m S_m}{N},$$

for $S_m \in [N - S_0, S_0]$. This implies that to have strict monotonicity we must have $\alpha \Delta t > 0$, which is the condition required for positivity (Theorem 9). Since we require positivity, we conclude that there are no other possible equilibrium points for Model III. □

### 3.1.4 Summary

We summarize the results for the positivity (Table 2), $R_0$ value (Table 3), and equilibrium points (Table 4) properties for the three discretized $SI$ models. We include in each table the numerical values used for the numerical simulations according to the parameter values set in Table 5.

| Model | Condition on $\alpha\Delta t$ | Numerically |
|---|---|---|
| I | $\alpha\Delta t \leq \min_n \left[\left(1+\frac{1}{2S_n}\right)\frac{N}{I_n}\right]$ | $\alpha\Delta t \leq \frac{250}{217}$ |
| II | $\alpha\Delta t < \min_n \left[\left(1+\frac{1}{S_n}\right)\frac{N}{I_n}\right]$ | $\alpha\Delta t < \frac{1000}{819}$ |
| III | $\alpha\Delta t \leq 1$ | $\alpha\Delta t \leq 1$ |
| Original | $\alpha\Delta t \leq 1$ | $\alpha\Delta t \leq 1$ |

Table 2: The condition on $\alpha\Delta t$ that guarantees the positivity property for the original and discrtetized $SI$ models. The numerical condition based on model simulation parameters in Table 5.

| Model | $R_0$ | Disease Spread | Numerically |
|---|---|---|---|
| I | $R_0 = \frac{2\alpha\Delta t I_0 S_0}{N}$ | $R_0 > 1 \quad \alpha\Delta t > \frac{N}{2I_0S_0}$ | $\alpha\Delta t > \frac{50}{99}$ |
| II | $R_0 = \frac{\alpha\Delta t I_0 S_0}{N}$ | $R_0 \geq 1 \quad \alpha\Delta t \geq \frac{N}{I_0S_0}$ | $\alpha\Delta t \geq \frac{100}{99}$ |
| III | no $R_0$ value | $\alpha\Delta t > 0$ | $\alpha\Delta t > 0$ |
| Original | no $R_0$ value | $\alpha\Delta t > 0$ | $\alpha\Delta t > 0$ |

Table 3: The $R_0$ value, if it exists, for the original and the discretized $SI$ models. The condition on $\alpha\Delta t$ that guarantees the disease spreads. The numerical condition based on model simulation parameters in Table 5.

| Model | $S_0 = N,\ I_0 = 0$ | $S_0 < N,\ I_0 > 0$ |
|---|---|---|
| I | $(N, 0)$ | $R_0 > 1 \quad (0, N)$<br>$R_0 \leq 1 \quad (S_0, I_0)$ |
| II | $(N, 0)$ | $R_0 \geq 1 \quad (0, N)$<br>$R_0 < 1 \quad (S_0, I_0)$ |
| III | $(N, 0)$ | $(0, N)$ |
| Original | $(N, 0)$ | $(0, N)$ |

Table 4: The equilibrium points for the original and the discretized $SI$ models.

# 4 Model Simulations

We ran trials of the original $SI$ epidemic model and the discretized $SI$ models using the program Mathematica. In each of these trials, most of the parameters were fixed in order to be able to appropriately compare results between different forms of discretizing. These parameters are summarized in Table 5. The only parameter that was altered for data analysis was $\alpha$. Since $\alpha$ is the parameter that determines how transmissible a disease is, changing $\alpha$ corresponds to considering a different disease. So we are considering different diseases spreading in the same population.

| Parameter | Description | Units | Value |
|---|---|---|---|
| $N$ | total population | people | 100 |
| $I_0$ | infectives | people | 1 |
| $S_0$ | susceptibles | people | 99 |
| $\Delta t$ | time step | time | 1 |
| $\alpha$ | contact rate | $(\text{time})^{-1}$ | variable |

Table 5: The description and units of the parameters of the $SI$ models. The parameter values used in numerical simulations.

For a disease with $\alpha = 0.67$, simulated using Model I, the $R_0$ value is larger than 1, and the numerical outputs include

$$S = \{99, 98, 97, 95, \dots\} \text{ and}$$
$$I = \{1, 2, 3, 5, \dots\}.$$

These outputs are indeed integers, they add up to the total population, $S_n + I_n = N$, and they are monotone. The equilibrium point $(0, 100)$ is reached at $n = 14$. Figure 1 shows the course of the disease for $n = 0$ through $n = 20$.

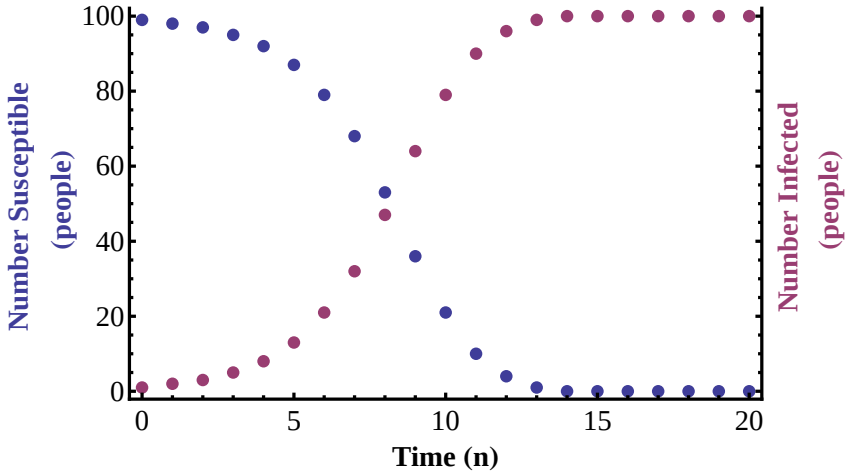


Figure 1: Model simulation for Model 1 (Round $S$, Round $I$) with $\alpha = 0.67$, and other parameter values as in Table 5.

For a disease with $\alpha = 0.25$, simulated using Model I, the $R_0$ value is less than 1, and the numerical outputs include

$$S = \{99, 99, 99, 99, \dots\} \text{ and}$$
$$I = \{1, 1, 1, 1, \dots\}.$$

These outputs are indeed integers, they add up to the total population, $S_n + I_n = N$, and they are monotone, however, the disease does not spread. The equilibrium point $(99, 1)$ is exactly the initial condition.

The original $SI$ model and both Model II and III have graphs similar to Figure 1, when $R_0 \geq 1$ in the case of Model II.

For a disease that spreads through the population, not all of the discretized models can be used. A particular disease corresponds to a particular transmission rate $\alpha$. Not every possible $\alpha$ can be used with each model due to the positivity condition and the $R_0$ value property.

# 5 Conclusion

We considered nine different discretized $SI$ models applying combinations of Round, Floor, and Ceiling to the original $SI$ epidemic model equations. Three cases satisfied the fundamental property of fixed population size. For each of the three successful discretized models,

we found the condition on $\alpha\Delta t$ that guarantees the positivity condition. We also found that Model I (Round $S$, Round $I$) and Model II (Ceiling $S$, Floor $I$) have a basic reproduction number, $R_0$, which gives a condition for when the disease will spread; the original $SI$ model and Model III (Floor $S$, Ceiling $I$) do not have such a condition. Finally, we determined the equilibrium points for the three discretized $SI$ models, which depend on the $R_0$ value. The equilibrium points are reached as outputs of the discretized models, unlike in the case of the original $SI$ model where they are approached asymptotically. These three discretized $SI$ models have provided us with a solution to the problem of the noninteger outputs of the original $SI$ model. Thus they fit our biological reality and offer better models for studying actual epidemics.

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